

In the Specification:

Please replace the paragraph beginning at page 144, line 13, as originally presented, with the following amended paragraph:

-- Quantitative RT-PCR was performed to measure expression levels of mouse IL-22RA in the colons of mice with DSS-induced IBD (Example 8). RNA was isolated from normal mouse colon and from the distal colons of DSS-treated mice from treatment days 2, 7 and 10. RT-PCR was performed using Applied Biosystems 7700 ~~TaqMan~~ TAQMAN® instrument and protocols. Briefly, "Primer Express" software was used to design primers against the mouse IL-22RA sequence (ZC39776 (SEQ ID NO:19) and ZC39777 (SEQ ID NO:20)) and a FAM/TAMRA labeled ~~TaqMan~~ TAQMAN® probe (ZC38752 (SEQ ID NO:21)) according to Applied Biosystems guidelines. 25ng of RNA was added to each reaction, along with PE/Applied Biosystems ~~TaqMan~~ TAQMAN® EZ RT-PCR Core Reagents and the above mentioned primers and probe. RT-PCR reactions were run in duplicate under the following conditions: 50°C for 2 minutes, 60°C for 30 minutes, 95°C for 5 minutes, 40 cycles of 94°C for 20 seconds and 60°C for 1 minute. Expression values were compared to a standard curve of known numbers of molecules of a synthetic mouse IL-22RA RNA transcript, and expression is reported as absolute number of molecules of mouse IL-22RA per reaction. Preliminary data suggests that mouse IL-22RA expression may be slightly down-regulated in the distal colons of day 7 and day 10 mice with DSS-induced IBD when compared to expression levels in normal mouse colon. --

Please replace the paragraph beginning at page 154, line 17, as originally presented, with the following amended paragraph:

-- Relative levels of IL-22 mRNA were determined by analyzing total RNA samples using the ~~TaqMan~~ TAQMAN® EZ RT-PCR Core Reagents Kit (PE Applied Biosystems). Runoff IL-22 transcript was made to generate a standard curve used for quantitation. The curve consisted of 10-fold serial dilutions ranging from about 1e8 to 1e3 total copies of whole message for IL-22 with each standard curve point analyzed in triplicate. The total RNA samples from skin were also analyzed in triplicate for human IL-22 transcript levels and for levels of hGUS as an endogenous control. In a total volume of 25 µl, each RNA sample was subjected to ~~TaqMan~~ TAQMAN® EZ RT-PCR reaction (PE Applied Biosystems) containing: approximately 25 ng of total RNA in DEPC treated water (Dnase/Rnase free); appropriate primers (approximately 800 nM ZC 42459 (SEQ ID NO:22) and ZC 42458 (SEQ ID NO:23); appropriate probe

(approximately 100 nM ZC 42460 (SEQ ID NO:24); 1X ~~TaqMan~~ TAQMAN® EZ Buffer; 3 mM Manganese acetate; 300 µM each d-CTP, d-ATP, and d-GTP and 600 µM of d-UTP; *rTth* DNA Polymerase (0.1 U/µl); and ~~AmpErase~~ AMPERASE® UNG (0.01 U/µl). PCR thermal cycling conditions were as follows: an initial UNG treatment step of one cycle at 50°C for 2 minutes; followed by a reverse transcription (RT) step of one cycle at 60°C for 30 minutes; followed by a deactivation of UNG step of one cycle at 95°C for 5 minutes; followed by 40 cycles of amplification at 94°C for 20 seconds and 60°C for 1 minute. --

Please replace the paragraph beginning at page 157, line 7, as originally presented, with the following amended paragraph:

-- Relative levels of IL-22 mRNA were determined by analyzing total RNA samples using the ~~TaqMan~~ TAQMAN® EZ RT-PCR Core Reagents Kit (PE Applied Biosystems). Runoff IL-22 transcript was made to generate a standard curve used for quantitation. The curve consisted of 10-fold serial dilutions ranging from about 1e8 to 1e3 total copies of whole message for IL-22 with each standard curve point analyzed in triplicate. The total RNA samples from skin were also analyzed in triplicate for human IL-22 transcript levels and for levels of hGUS as an endogenous control. In a total volume of 25 µl, each RNA sample was subjected to ~~TaqMan~~ TAQMAN® EZ RT-PCR reaction (PE Applied Biosystems) containing: approximately 25 ng of total RNA in DEPC treated water (Dnase/Rnase free); appropriate primers (approximately 800 nM ZC 42459 (SEQ ID NO:22) and ZC 42458 (SEQ ID NO:23); appropriate probe (approximately 100 nM ZC 42460 (SEQ ID NO:24); 1X ~~TaqMan~~ TAQMAN® EZ Buffer; 3 mM Manganese acetate; 300 µM each d-CTP, d-ATP, and d-GTP and 600 µM of d-UTP; *rTth* DNA Polymerase (0.1 U/µl); and ~~AmpErase~~ AMPERASE® UNG (0.01 U/µl). PCR thermal cycling conditions were as follows: an initial UNG treatment step of one cycle at 50°C for 2 minutes; followed by a reverse transcription (RT) step of one cycle at 60°C for 30 minutes; followed by a deactivation of UNG step of one cycle at 95°C for 5 minutes; followed by 40 cycles of amplification at 94°C for 20 seconds and 60°C for 1 minute. --

Please replace the paragraph beginning at page 169, line 3, as originally presented, with the following amended paragraph:

-- Relative levels of IL-20 mRNA were determined by analyzing total RNA samples using the ~~TaqMan~~ TAQMAN® EZ RT-PCR Core Reagents Kit (PE Applied Biosystems). Runoff IL-20 transcript was made to generate a standard curve

used for quantitation. The curve consisted of 10-fold serial dilutions ranging from about 1e8 to 1e3 total copies of whole message for IL-20 with each standard curve point analyzed in triplicate. The total RNA samples from skin were also analyzed in triplicate for human IL-20 transcript levels and for levels of hGUS as an endogenous control. In a total volume of 25 µl, each RNA sample was subjected to ~~TaqMan~~ TAQMAN® EZ RT-PCR reaction (PE Applied Biosystems) containing: approximately 25 ng of total RNA in DEPC treated water (Dnase/Rnase free); appropriate primers (approximately 800 nM ZC40541 (SEQ ID NO:25) and ZC40542 (SEQ ID NO:26); appropriate probe (approximately 100 nM ZC40544 (SEQ ID NO:27); 1X ~~TaqMan~~ TAQMAN® EZ Buffer; 3 mM Manganese acetate; 300 µM each d-CTP, d-ATP, and d-GTP and 600 µM of d-UTP; *rTth* DNA Polymerase (0.1 U/µl); and ~~AmpErase~~ AMPERASE® UNG (0.01 U/µl). PCR thermal cycling conditions were as follows: an initial UNG treatment step of one cycle at 50°C for 2 minutes; followed by a reverse transcription (RT) step of one cycle at 60°C for 30 minutes; followed by a deactivation of UNG step of one cycle at 95°C for 5 minutes; followed by 40 cycles of amplification at 94°C for 20 seconds and 60°C for 1 minute. --

Please replace the paragraph beginning at page 171, line 18, as originally presented, with the following amended paragraph:

-- Relative levels of IL-20 mRNA were determined by analyzing total RNA samples using the ~~TaqMan~~ TAQMAN® EZ RT-PCR Core Reagents Kit (PE Applied Biosystems). Runoff IL-20 transcript was made to generate a standard curve used for quantitation. The curve consisted of 10-fold serial dilutions ranging from about 1e8 to 1e3 total copies of whole message for IL-20 with each standard curve point analyzed in triplicate. The total RNA samples from skin were also analyzed in triplicate for human IL-20 transcript levels and for levels of hGUS as an endogenous control. In a total volume of 25 µl, each RNA sample was subjected to ~~TaqMan~~ TAQMAN® EZ RT-PCR reaction (PE Applied Biosystems) containing: approximately 25 ng of total RNA in DEPC treated water (Dnase/Rnase free); appropriate primers (approximately 800 nM ZC40541 (SEQ ID NO:25) and ZC40542 (SEQ ID NO:26); appropriate probe (approximately 100 nM ZC40544 (SEQ ID NO:27); 1X ~~TaqMan~~ TAQMAN® EZ Buffer; 3 mM Manganese acetate; 300 µM each d-CTP, d-ATP, and d-GTP and 600 µM of d-UTP; *rTth* DNA Polymerase (0.1 U/µl); and ~~AmpErase~~ AMPERASE® UNG (0.01 U/µl). PCR thermal cycling conditions were as follows: an initial UNG treatment step of one cycle at 50°C for 2 minutes; followed by a reverse transcription (RT) step of one cycle at 60°C for 30 minutes; followed by a deactivation of UNG step of one cycle at

95°C for 5 minutes; followed by 40 cycles of amplification at 94°C for 20 seconds and 60°C for 1 minute. --